FIG. 1A-1

```
10         20         30         40         50         60         70
GGAGGTATAGGAGCTCTCTTCGATTTTAGCAAACCAGGAGTCCGAAGATCTAAGGAGAGCTGGGGGTTTGACTCC
           SacI                                    BglII
          85         95        105        115        125        135        145
GAGAGCTCGAGCAGTCCCCAAGACCTGGTCTTGACTCACGAGTTAGACTCCACTCAGAGGCTGACTGTCTCCAGG
  SacI             PflMI
     XhoI               TthlllI
          160        170        180        190        200        210        220
GTCTACACCTCTAAGGGCGACACTGGGCTCAAGCAGACTGCCGTTTTCTATATGGGATGAGCCTTCACAGGGCAG
          235        245        255        265        275        285        295
CCAGTTGGGATGGGTTGAGGTTTGGCTGTAGACATCAGAAACCCAAGTCAAATGCGCTTCAACCAGTAGAAAATT
          310        320        330        340        350        360        370
CACCAGCCCGCAGAGCTAAGGTTGGGTGGACATTAGGGTTGGTTGATCCAGGAGCTCAACAGTGTCCTCTGAGCC
                                                      SacI
          385        395        405        415        425        435        445
CCAGCTCCTTCTGCCCCACCCCACCATCTTCAGTGCTGCTTCCTCTCAAGGCCACAGCTGTAGTTGGCCAGGGGG
                                                   PvuII      BalI
                                                                BglI
          460        470        480        490        500        510        520
GCTTCATTATTTTTTGCTCCTGGGCAGTAGGAGGAAGAGAATGAATGTCTCTCCATGGGTCTTTCTTAGGAATGT
                                                      NcoI
          535        545        555        565        575        585        595
GGGAACTTTTTCCAGAAGTCTCTATGTCTTTTAGTTTGTGTTGGGTCACTTGCCCTTCCTGAACCACTTCCTGAC
          610        620        630        640        650        660        670
TCCTGGACAGGATGTGCACTGATGAGCTTAGCTTTGGGGATCTAATAGTGACTTTACAAAGCCTCTTTGAGAAGG
              ApaLI      EspI
          685        695        705        715        725        735        745
TGACATTGGAACCAAGGCTTGAGCAGACACAACAAAGATTGCAGGGAGGGGCATTGCAGGTGGAGGAAACGGCAC
                                                   BspMI-
          760        770        780        790        800        810        820
ATGCAAGAGCCCTGCGTGGGAGTGAGCTTGGTGTTTGGTCAATCAGTTGTCAGAGCACACCGGGCCCTGTCAGCA
                                                            ApaI
                                                            EcoO
```

FIG. 1A-2

```
835       845       855       865       875       885       895
GGCACAGCCTGGGCCTGCTCTGAGTATGACAGAGAGCCCCTGGGAAGTTGTAGGTGGAGGAAAGACAGGTCATGA
          910       920       930       940       950       960       970
CTAGGAAAAAAGCAATCCCTCTGTTGTGGGGTGGAAGGAAGGTTGCAGTGTGTGTGAGAGAGAGACAAGACAGAC
          985       995       1005      1015      1025      1035      1045
AGACAGACACTTCTCAATGTTTACAAGTGCTCAGGCCCTGACCCGAATGCTTCCAAATTTACGTAGTTCTGGAAA
                                    EcoO      BsmI+          SnaBI
          1060      1070      1080      1090      1100      1110      1120
ACCCCCTGTATCATTTTCACTACTCAAAGAAACCTCGGGAGTGTTTTCTTCTGAAAGGTCATCAGGTTTTGACTC
          1135      1145      1155      1165      1175      1185      1195
TCTGCTGTCTCATTTCTTCTTGCTGGTGGTGGTGATGGTTGCTTGTCCCAGGCCCTGTCCCGCATCCTCTTGCCC
                                                EcoO
          1210      1220      1230      1240      1250      1260      1270
CTGCAGAGGGATGAGTGTGTTGGGGCCTCACGAGTTGAGGTTGTTCATAAGCAGATCTCTTTGAGCAGGGCGCCT
PstI                EcoO                                BglII           NarI Ps
          1285      1295      1305      1315      1325      1335      1345
GCAGTGGCCTTGTGTGAGGCTGGAGGGGTTTCGATTCCCTTATGGAATCCAGGCAGATGTAGCATTTAAACAACA
tI                                                                  DraI
          1360      1370      1380      1390      1400      1410      1420
CACGTGTATAAAAGAAACCAGTGTCCGCAGAAGGTTCCAGAAAGTATTATGGGATAAGACTACATGAGAGAGGAA
          1435      1445      1455      1465      1475      1485      1495
TGGGGCATTGGCACCTCCCTTAGTAGGGCCTTTGCTGGGGGTAGAAATGAGTTTTAAGGCAGGTTAGACCCTCGA
                          EcoO                              BspMI-
          1510      1520      1530      1540      1550      1560      1570
ACTGGCTTTTGAATCGGGAAATTTACCCCCCAGCCGTTCTGTGCTTCATTGCTGTTCACATCACTGCCTAAGATG
          1585      1595      1605      1615      1625      1635      1645
GAGGAACTTTGATGTGTGTGTGTTTCTTTCTCCTCACTGGGCTCTGCTTCTTCACTTCCTTGTCAATGCAGAGAA
          1660      1670      1680      1690      1700      1710      1720
CAGCAGCAGGCACCAGAGGCAGGCCTTGTAAGAAGCACGAGCTGTATGTCAGCTTCCGAGACCTGGGCTGGCAGG
                    StuI                                                BspMI
          1735      1745      1755      1765      1775      1785      1795
TAAGGGGCTGGCTGGGTCTGTCTTGGGTGTGGGCCCTCTGGCGTGGGCTCCCACAGGCAGCGGGTGCTGTGCTCA
                                ApaI
                                EcoO
```

FIG. 1A-3

```
        1810      1820      1830      1840      1850      1860      1870
GTCTTGTTTCTCATCTCTGCCAGTTAAGACTCCAGTATCAAGTGGCCTCGCTAGGGAAGGGTACTTGGCTAAGGA
        1885      1895      1905      1915      1925      1935      1945
TACAGGG.......(APPROX. 1000 BASES).............GGGAGCCAGCATGGGTGATGCCATTATGA
        1960      1970      1980      1990      2000      2010      2020
GTTATTAGCCTCTCTGGCAGGTGGGCAAACCGAGGCATGGAGGTTTGTTTAAGGTGAACTGCCAGTGTGTGACCA
      BglI     BspMI-                                                    Dr
                                                                         Pfl
        2035      2045      2055      2065      2075      2085      2095
CCTAGTGGGGTAGAGCTGATGATTGCCTCACACCGGAGCTCCTTCCTGTGCCGCGTTCTGTCCAGAAGACACAGC
aIII                                  SacI                              N
MI
        2110      2120      2130      2140      2150      2160      2170
CATGGATGTCCATTTTAGGATCAGCCAAGCCCCGTCTTGTCCTTCATTTTTATTTTATGTTTTTTTAGAAATGGG
coI
        2185      2195      2205      2215      2225      2235      2245
GTCTTGCTCTGTCACCCAGGCTGGGTGCAGTGGTGTGATCATAGCTCACCGCAGCTTTGACGCCGTCTTCCCACT
                                                              TthlllI
        2260      2270      2280      2290      2300      2310      2320
CAGTCTACTAAGCTTGGACTATAGGCCAAGACTATAGAGTGGTCCTTCTTTCCATTCTTTTGGGACCATGAGAGG
       HindIII                                        BstXI
        2335      2345      2355      2365      2375      2385      2395
CCACCCATGTTTCCTGCCCCTGCTGGGCCCTGCTGCTCAGAAGGCATGGTCTGAGGCTTTCACCTTGGTCGTGAG
                        ApaI
                        EcoO
        2410      2420      2430      2440      2450      2460      2470
CCTTCGTGGTGGTTTCTTTCAGCATGGGGTTGGGATGCTGTGCTCAGGCTTCTGCATGGTTTCCCACACTCTCTT
        2485      2495      2505      2515      2525      2535      2545
CTCCTCCTCAGGACTGGATCATCGCGCCTGAAGGCTACGCGCGCTACTACTGTGAGGGGGAGTGTGCCTTCCCTC
    MstII                                 BssHII
        2560      2570      2580      2590      2600      2610      2620
TGAACTCCTACATGAACGCCACCAACCACGCCATCGTGCAGACGCTGGTGGGTGTCACGCCATCTTGGGGTGTGG
                                                                        Bs
        2635      2645      2655      2665      2675      2685      2695
TCACCTGGGCCGGGCAGGCTGCGGGGCCACCAGATCCTGCTGCCTCCAAGCTGGGGCCTGAGTAGATGTCAGCCC
tEII    BglI                                          EcoO
```

FIG. 1A-4

```
                2710       2720       2730       2740       2750       2760       2770
ATTGCCATGTCATGACTTTTGGGGGCCCCTTGCGCCGTTAAAAAAAAATCAAAAATTGTACTTTATGACTGGTTT
                           ApaI
                           EcoO
                2785       2795       2805       2815       2825       2835       2845
GGTATAAAGAGGAGTATAATCTTCGACCCTGGAGTTCATTTATTTCTCCTAATTTTTAAAGTAACTAAAAGTTGT
                                                                  DraI
                2860       2870       2880       2890       2900       2910       2920
ATGGGCTCCTTTGAGGATGCTTGTAGTATTGTGGGTGCTGGTTACGGTGCCTAAGAGCACTGGGCCCCTGCTTCA
                                                                  ApaI
                                                                  EcoO
                2935       2945       2955       2965       2975       2985       2995
TTTTCCAGTAGAGGAAACAGGTAAACAGATGAGAAATTTCAGTGAGGGGCACAGTGATCAGAAGCGGGCCAGCAG
                3010       3020       3030       3040       3050       3060       3070
GATAATGGGATGGAGAGATGAGTGGGGACCCATGGGCCATTTCAAGTTAAATTTCAGTCGGGTCACCAGGAAGAT
                           EcoO NcoI                                   BstEII
                3085       3095       3105       3115       3125       3135       3145
TCCATGTGATAATGAGATTAACGTGCCCAGTCACGGCGACACTCAGTAGGTGTTATTCCTGCTCTGCCAACAGCA
                3160       3170       3180       3190       3200       3210       3220
ACCATAGTTGATAAGAGCTGTTAGGGATTTTGTCCTTTTGCTTAGAATCCAAGGTTCAAGGACCTTGGTTATGTA
                                                                  EcoO
                3235       3245       3255       3265       3275       3285       3295
GCTCCCTGTCATGAACATCATCTGAGCCTTTCCTGCCTACTGATCATCCACCCTGCCTTGAATGCTTCTAGTGAC
                                                                  BsmI+
                3310       3320       3330       3340       3350       3360       3370
AGAGAGCTCACTACCAGGACTACTCCCTCCTTTCATTTAGTAATCTGCCTCCTTCTTTTCTTGTCCCTGTCCTGT
   SacI
                3385       3395       3405       3415       3425       3435       3445
GTGTTAAGTCCTGGAGAAAAATCTCATCTATCCCTTTCATTTGATTCTGCTCTTTGAGGGCAGGGGTTTTTGTTT
                3460       3470       3480       3490       3500       3510       3520
CTTTGTTTGTTTTTTTAAGTGTTGGTTTTCCAAAGCCCTTGCTCCCCTCCTCAATTGAAACTTCAAAGCCCTCAT
                3535       3545       3555       3565       3575       3585       3595
TGGGATTGAAGGTCCTTAGGCTGGAAACAGAAGAGTCCTCCCCAACCTGTTCCCTGGCCTGGATGTGCTGTGCTG
          EcoOMstII
```

FIG. 1A-5

```
                3610       3620       3630       3640       3650       3660       3670
TGCCAGTATCCCCTGGAAGGTGCCAGGCATGTCTCCCCGGCTGCCAGGGGACACATCTCTATCCTTCTCCAACCC
                3685       3695       3705       3715       3725       3735       3745
CTGCCTTCATGGCCCATGGAACAGGAGTGCCATCGCCCTGTGTGCACCTACTTCCATCAGTATTTCACCAGAGAT
  BglI        NcoI                                 ApaLI                          BglI
                  3760       3770       3780       3790       3800       3810       3820
CTGCAGGATCAAAGTGAATTCTCCAGGGATTGTGAAATGATGCGATTGTGGTCATGTTTAAAAGGGGGCAACTGT
I                    EcoRI                                          DraI
PstI
                3835       3845       3855       3865       3875       3885       3895
CTTCTAGAGAGTCCTGATGAAATGCTTCCAGAGGAAATGAGCTGATGGCTGGAATTTGCTTTAAAATCATTCAAG
  XbaI                                                                 DraI
                3910       3920       3930       3940       3950       3960       3970
GTGGAGCAGGTGGGGAAGGGTATGGATGTGTAAGAGTTTGAAATTGTCCATCATAAAATGTGTAAAAAGCATGCT
     BspMI-                                                                    SphI
                3985       3995       4005       4015       4025       4035       4045
GGCCTATGTCAGCAGTCACAGCCTGGAGGTGGTAACAGAGTGCCAGTCACTGATGCTCAAGCCTGGCACCTACAG
                4060       4070       4080       4090       4100       4110       4120
TTGCTGGAAACCCAGAAGTTTCACGTTGAAAACAACAGGACAGTGGAATCTCTGGCCCTGTCTTGAACACGTGGC
                4135       4145       4155       4165       4175       4185       4195
AGATCTGCTAACACTGATCTTGGTTGGCTGCCGTCAGCTTAGGTTGAGTGGCGGTCTTCCCTTAGTTTGCTTAGT
BglII
                4210       4220       4230       4240       4250       4260       4270
CCCCGCTATTCCCTATTGTCTTACCTCGGTCTATTTTGCTTATCAGTGGACCTCACGAGGCACTCATAGGCATTT
                4285       4295       4305       4315       4325       4335       4345
GAGTCTATGTGTCCCTGTCCCACATCCTCTGTAAGGTGCAGAGAAGTCCATGAGCAAGATGGAGCACTTCTAGTG
                4360       4370       4380       4390       4400       4410       4420
GGTCCAAGTCAGGGACACTATTCAGCAATCTACAGTGCACAGGGCAGTTCCCCAACAGAGAATTACCTGGTCCTG
                                        ApaLI
                4435       4445       4455       4465       4475       4485       4495
AATGTCGGATCTGGCCCCTTCCTTCCCCACTGTATAATGTGAAAACCTCTATGCTTTGTTCCCCTTGTCTGCAAA
                4510       4520       4530       4540       4550       4560       4570
ACAGGGATAATCCCAGAACTGAGTTGTCCATGTAAAGTGCTTAGAACAGGGAGTGCTTGGCTTGGGGAGTGTCAC
                                                                              Bs
```

FIG. 1A-6

```
        4585       4595       4605       4615       4625       4635       4645
CTGCAGTCATTCATTATGCCCAGACAGGATGTTTCTTTATAGAAACGTGGAGGCCAGTTAGAACGACTCACCGCT
pMI+
PstI
        4660       4670       4680       4690       4700       4710       4720
TCTCACCACTGCCCATGTTTTGGTGTGTGTTTCAGGTCCACTTCATCAACCCGGAAACGGTGCCCAAGCCCTGCT
             PflMI
        4735       4745       4755       4765       4775       4785       4795
GTGCGCCCACGCAGCTCAATGCCATCTCCGTCCTCTACTTCGATGACAGCTCCAACGTCATCCTGAAGAAATACA
        4810       4820       4830       4840
GAAACATGGTGGTCCGGGCCTGTGGCTGCCACTAGCTCCTCCGA
```

FIG. 1B

```
CONSENSUS PROBE   20        30        40        50        60        70
GATCCTAATGGGCTGTACGTGGACTTCCAGCGCGACGTGGGCTGGGACGACTGGATCATCGCCCCCGTCG
      **                          ** *** ********   ************** **
TGTAAGAAGCACGAGCTGTATGTCAGCTTCCGAGACCTGGGCTGGCAGGACTGGATCATCGCGCCTGAAG
OP4     28        38        48        58        68        78        88

        80        90        100       110       120       130       140
ACTTCGACGCCTACTACTGCTCCGGAGCCTGCCAGTTCCCCTCTGCGGATCACTTCAACAGCACCAACCA
 ** **    *********    **    **    *****           **   ***  *********
GCTACGCGCGCTACTACTGTGAGGGGGAGTGTGCCTTCCCTCTGAACTCCTACATGAACGCCACCAACCA
        98        108       118       128       138       148       158

        150       160       170       180       190       200       210
CGCCGTGGTGCAGACCCTGGTGAACAACATGAACCCCGGCAAGGTACCCAAGCCCTGCTGCGTGCCCACC
****   ******** *****  **  *** *****      *** **************   ******
CGCCATCGTGCAGACGCTGGTCCACTTCATCAACCCGGAAACGGTGCCCAAGCCCTGCTGTGCGCCCACG
        168       178       188       198       208       218       228

        220       230       240       250       260       270       280
GAGCTGTCCGCCATCAGCATGCTGTACCTGGACGAGAATTCCACCGTGGTGCTGAAGAACTACCAGGAGA
 ****    ******       ** ***   ** **    **** ***    ******** ***       *
CAGCTCAATGCCATCTCCGTCCTCTACTTCGATGACAGCTCCAACGTCATCCTGAAGAAATACAGAAACA
        238       248       258       268       278       288       298

        290       300       310
TGACCGTGGTGGGCTGCGGCTGCCGCTAACTGCA
**   **   ** *** ******* *** **
TGGTGGTCCGGGCCTGTGGCTGCCACTAGCTCCT
        308       318       328
```

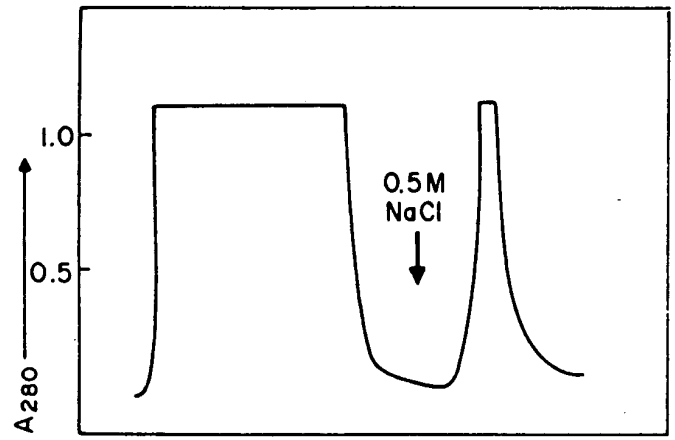


FIG. 2A

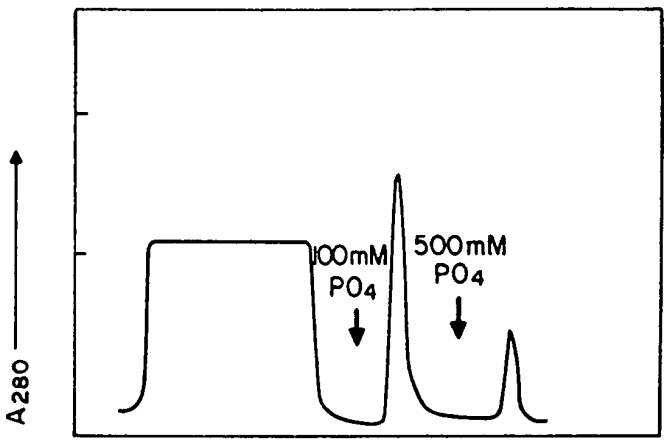
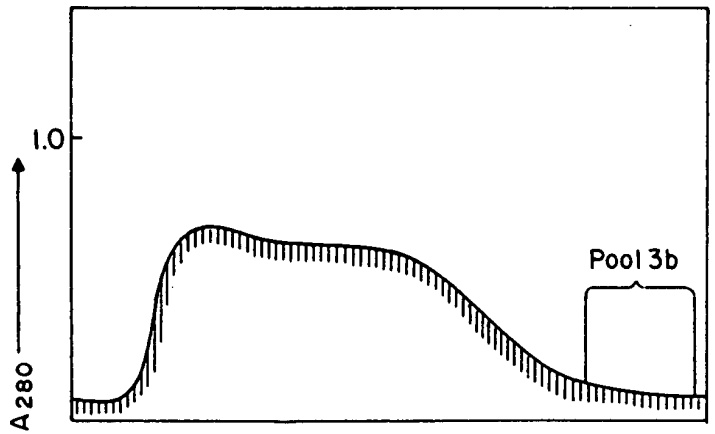
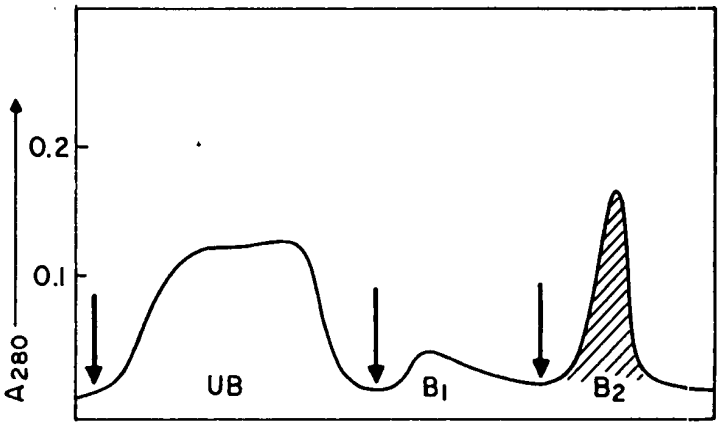


FIG. 2B



BUFFER: 4M GUANIDINE HCl, 50mM TRIS, PH 7.0

FIG. 2C



UB: 6M UREA 50mM TRIS 0.1M NaCl PH 7.0
B_1: 6M UREA 50mM TRIS 0.15M NaCl PH 7.0
B_2: 6M UREA 50mM TRIS 0.5M NaCl PH 7.0

FIG. 2D

FIG. 3A FIG. 3B

FIG. 4A FIG. 4B

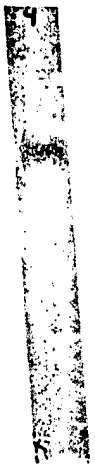
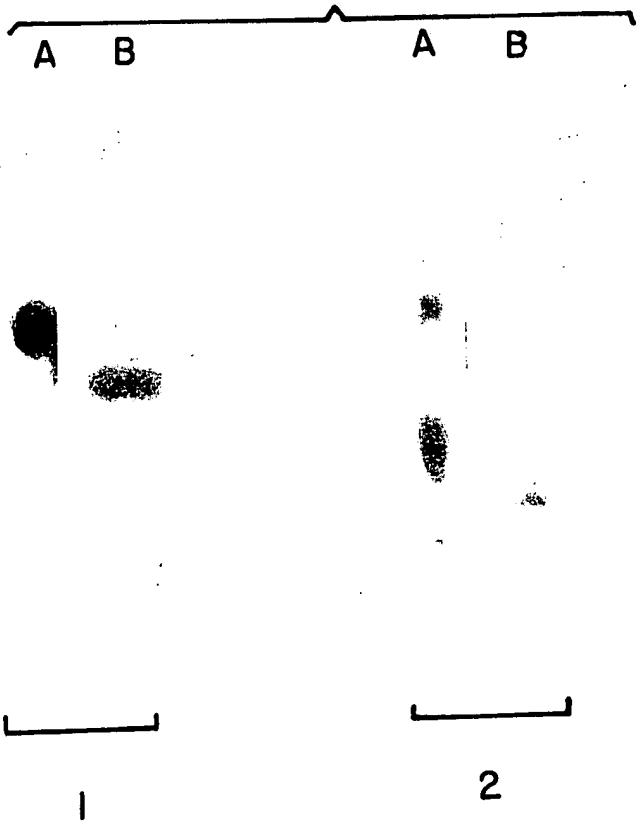


FIG. 5



365 88612388

FIG. 6 A FIG. 6 B FIG. 6 C FIG. 6 D FIG. 6 E

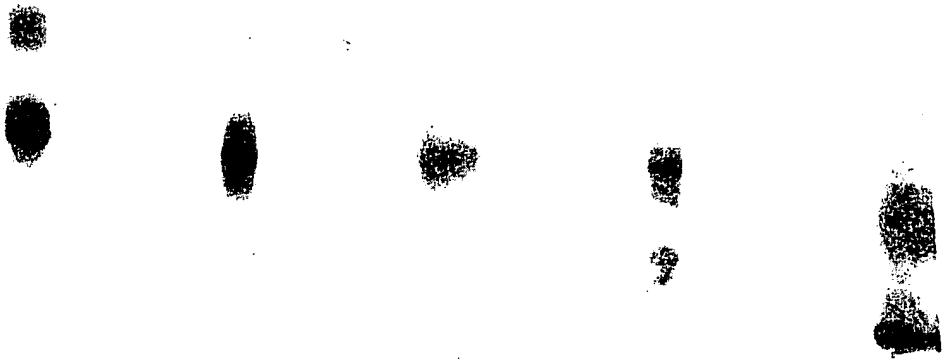
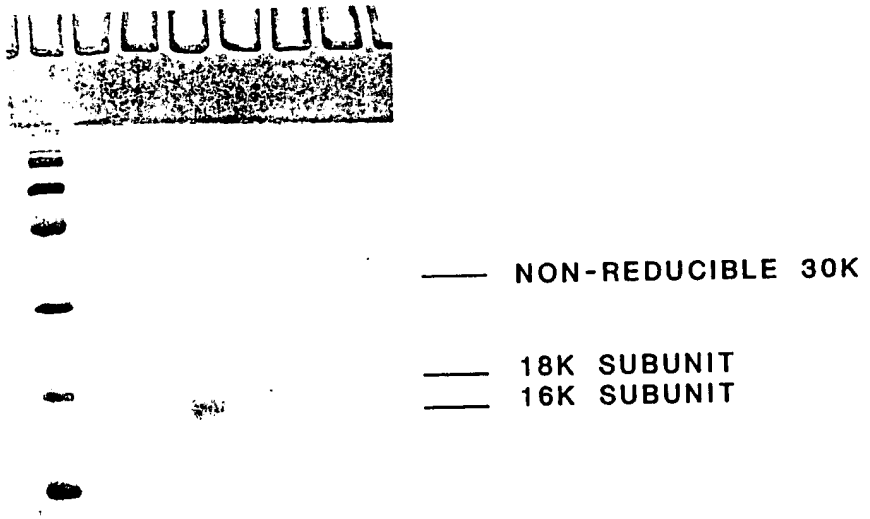


FIG. 15



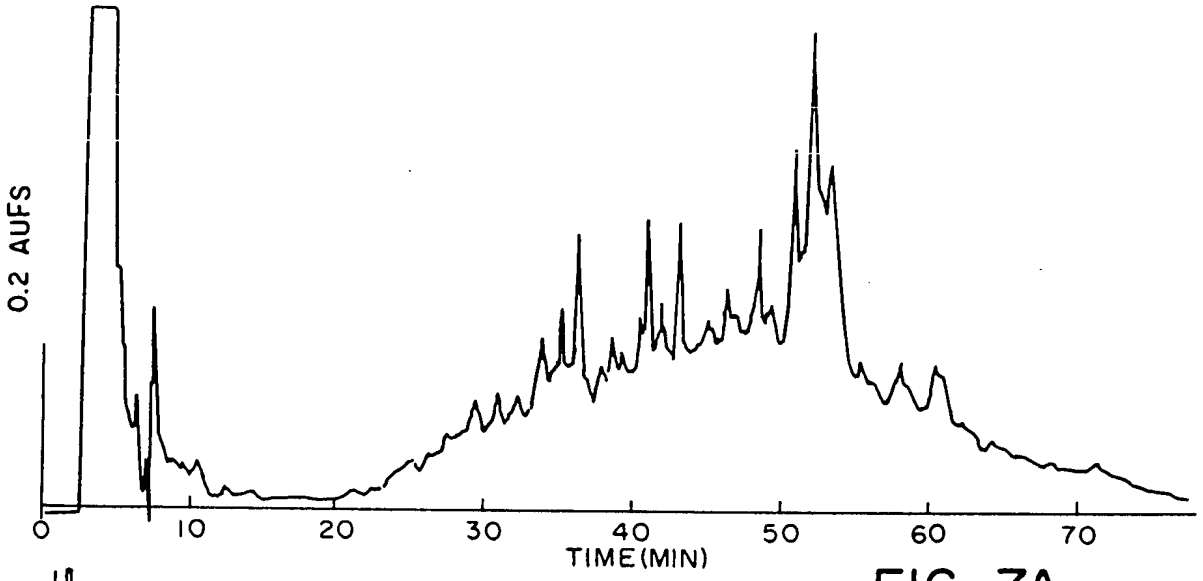


FIG. 7A

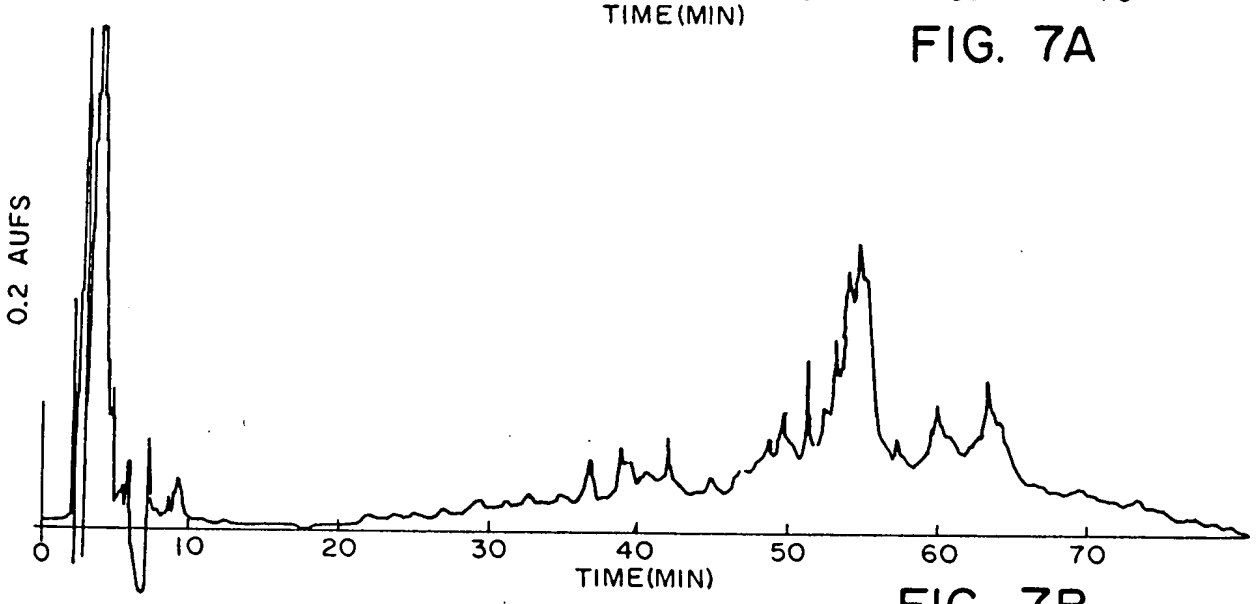


FIG. 7B

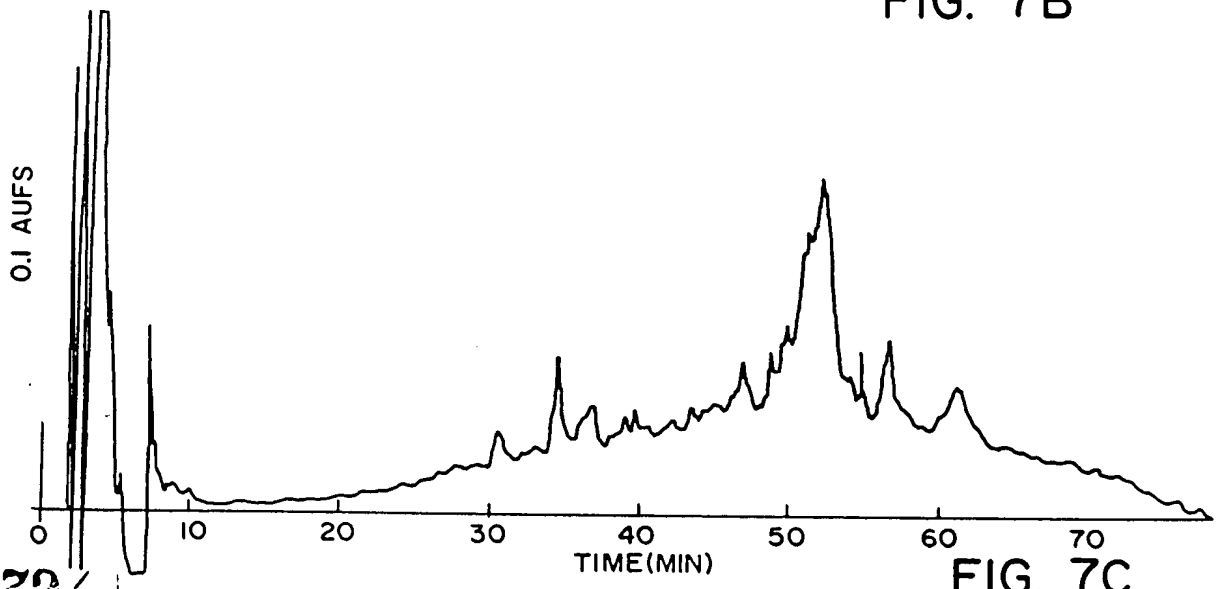


FIG. 7C

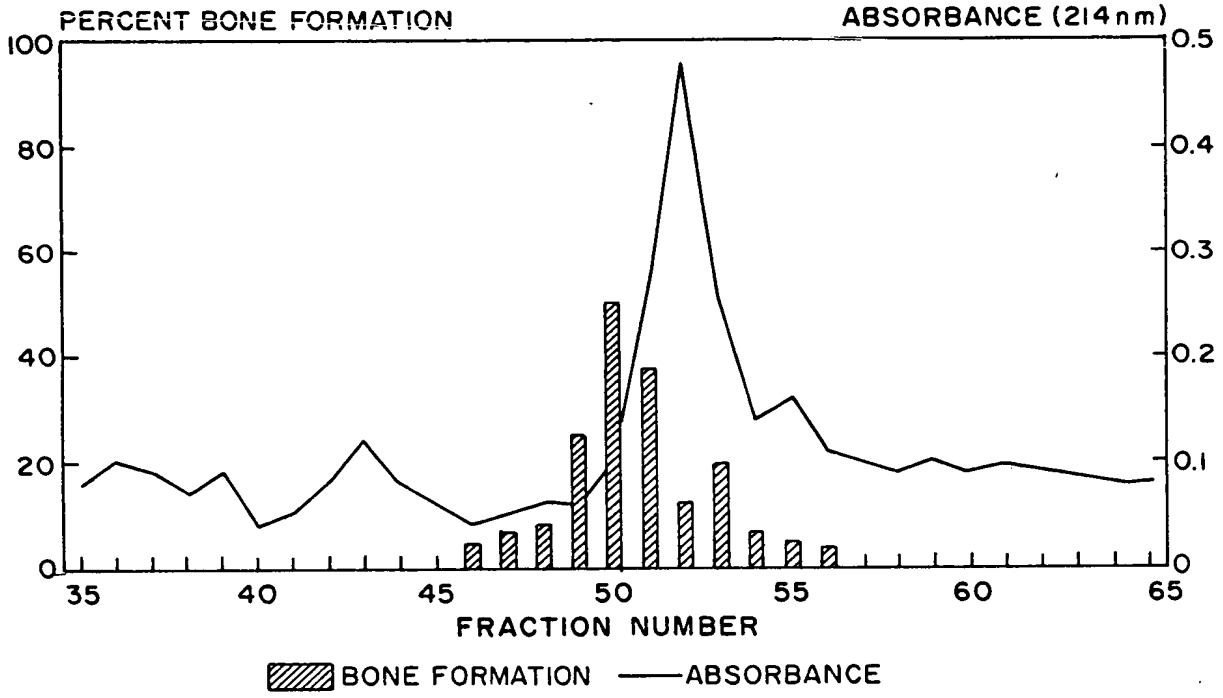


FIG. 8

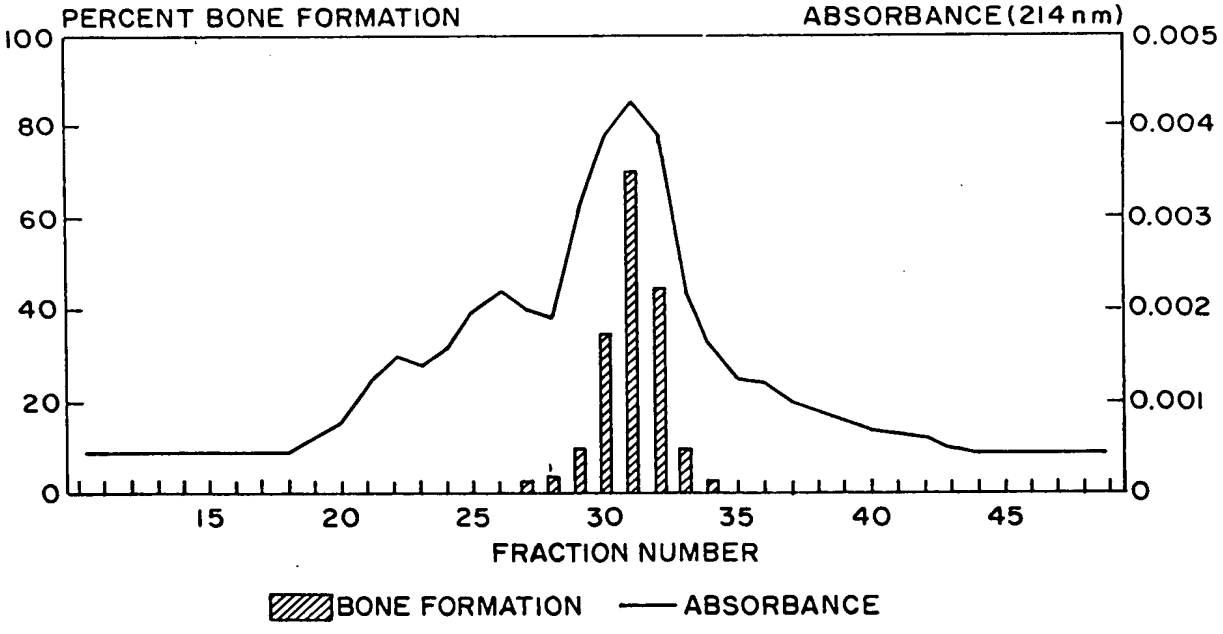


FIG. 9

07/821988

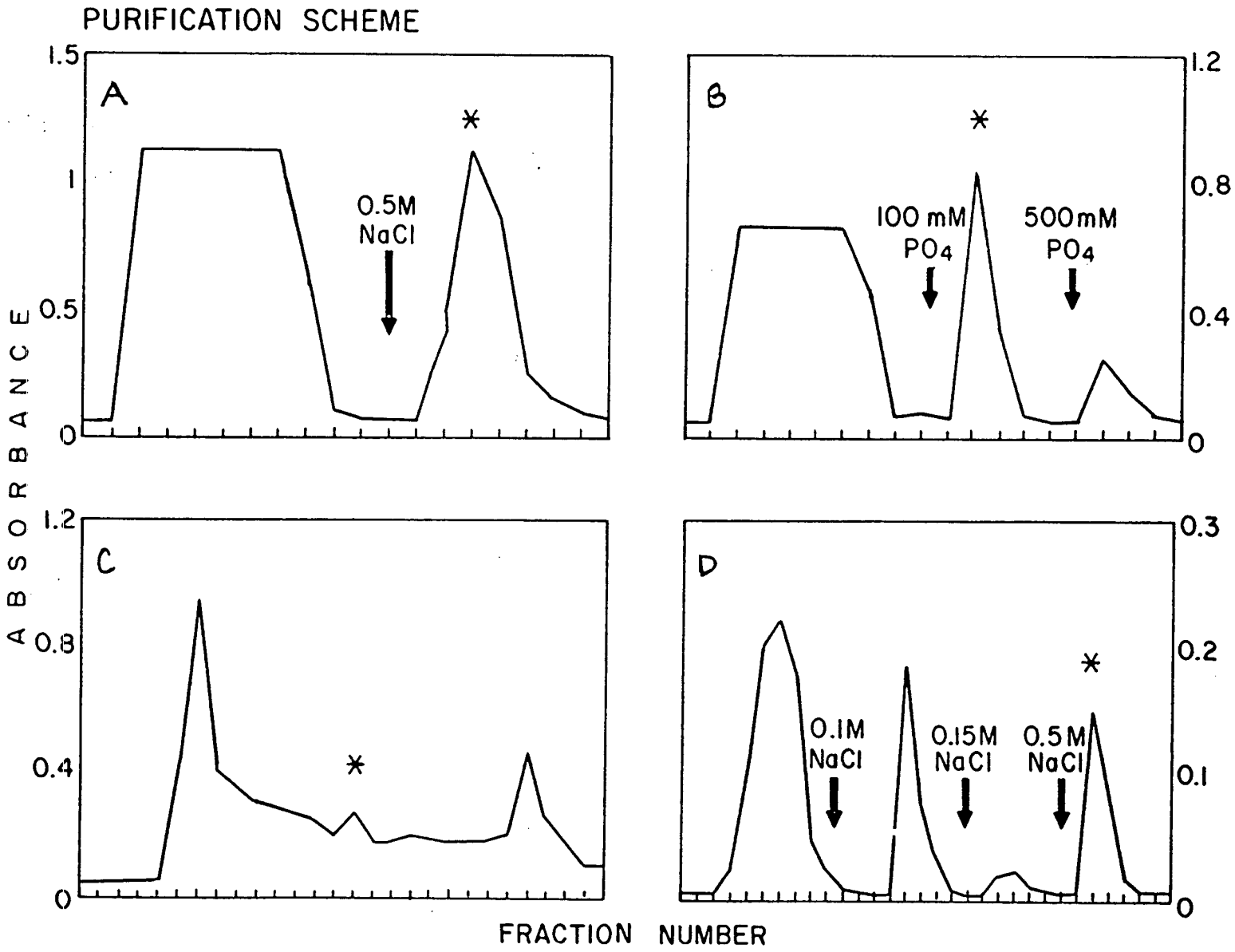


FIG. 10

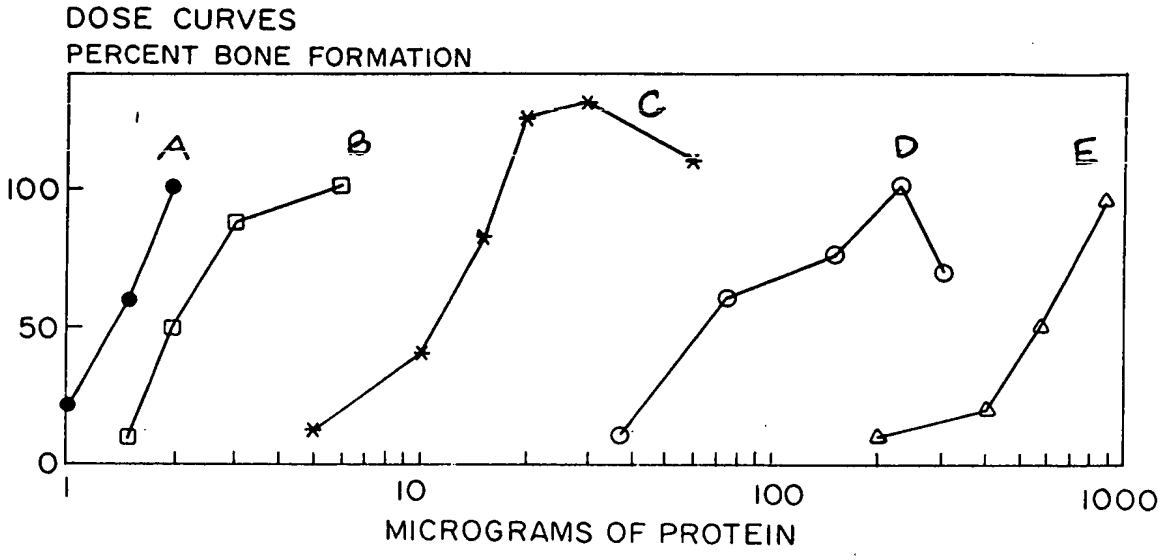


FIG. 11

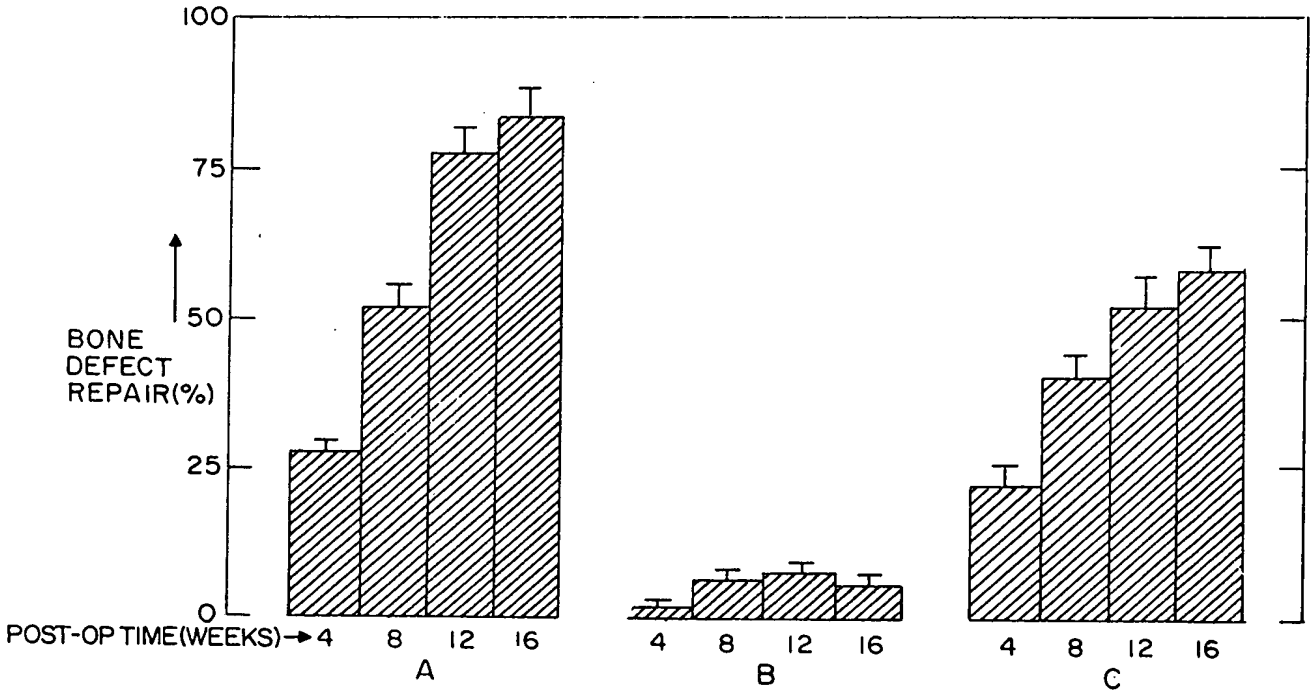


FIG. 12

FIG. 13

```
        10         20         30         40         50
GATCCTAATGGGCTGTACGTGGACTTCCAGCGCGACGTGGGCTGGGACGA
 D  P  N  G  L  Y  V  D  F  Q  R  D  V  G  W  D  D

        60         70         80         90        100
CTGGATCATCGCCCCCGTCGACTTCGACGCCTACTACTGCTCCGGAGCCT
  W  I  I  A  P  V  D  F  D  A  Y  Y  C  S  G  A

       110        120        130        140        150
GCCAGTTCCCCTCTGCGGATCACTTCAACAGCACCAACCACGCCGTGGTG
C  Q  F  P  S  A  D  H  F  N  S  T  N  H  A  V  V

       160        170        180        190        200
CAGACCCTGGTGAACAACATGAACCCCGGCAAGGTACCCAAGCCCTGCTG
 Q  T  L  V  N  N  M  N  P  G  K  V  P  K  P  C  C

       210        220        230        240        250
CGTGCCCACCGAGCTGTCCGCCATCAGCATGCTGTACCTGGACGAGAATT
  V  P  T  E  L  S  A  I  S  M  L  Y  L  D  E  N

       260        270        280        290        300
CCACCGTGGTGCTGAAGAACTACCAGGAGATGACCGTGGTGGGCTGCGGC
S  T  V  V  L  K  N  Y  Q  E  M  T  V  V  G  C  G

       310
TGCCGCTAACTGCAG
 C  R  *
```

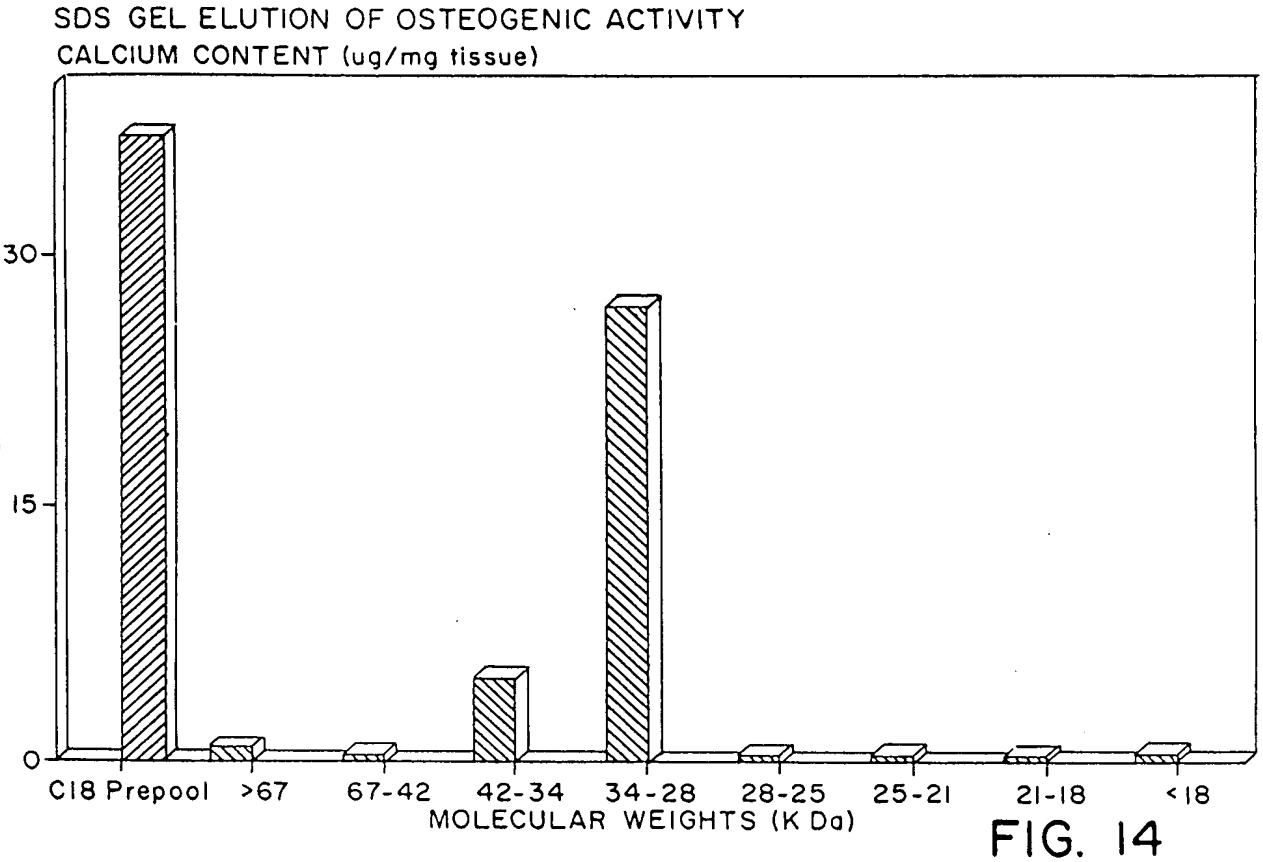


FIG. 14

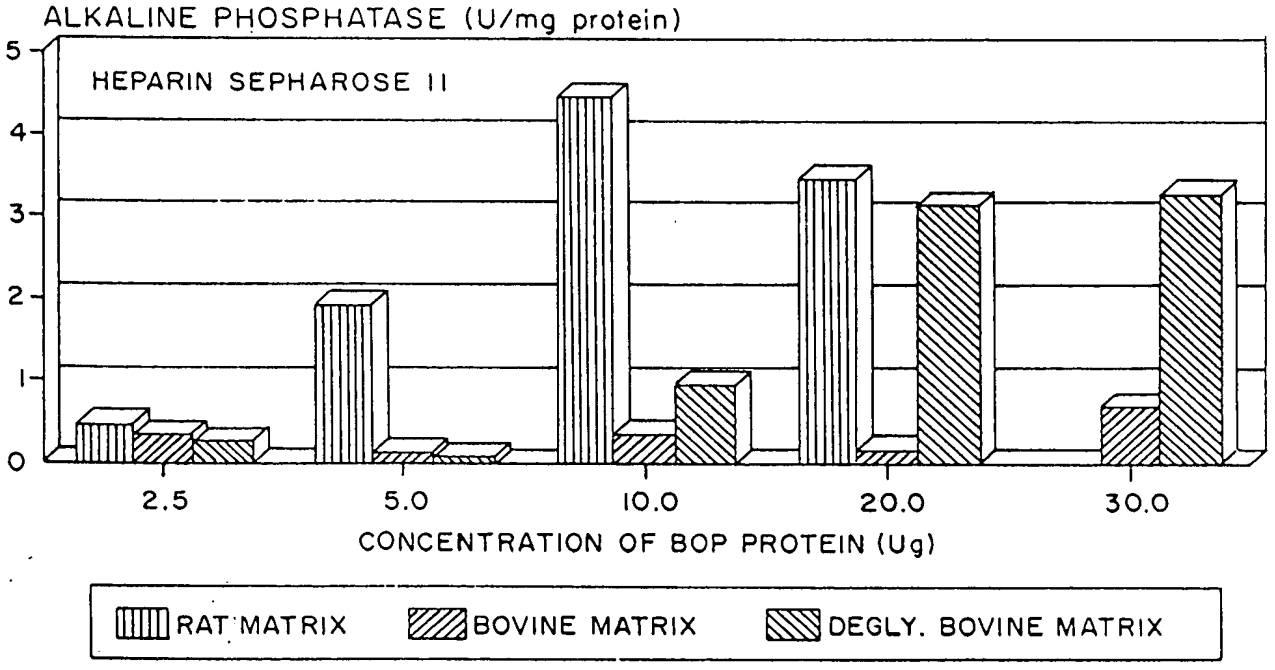


FIG. 19

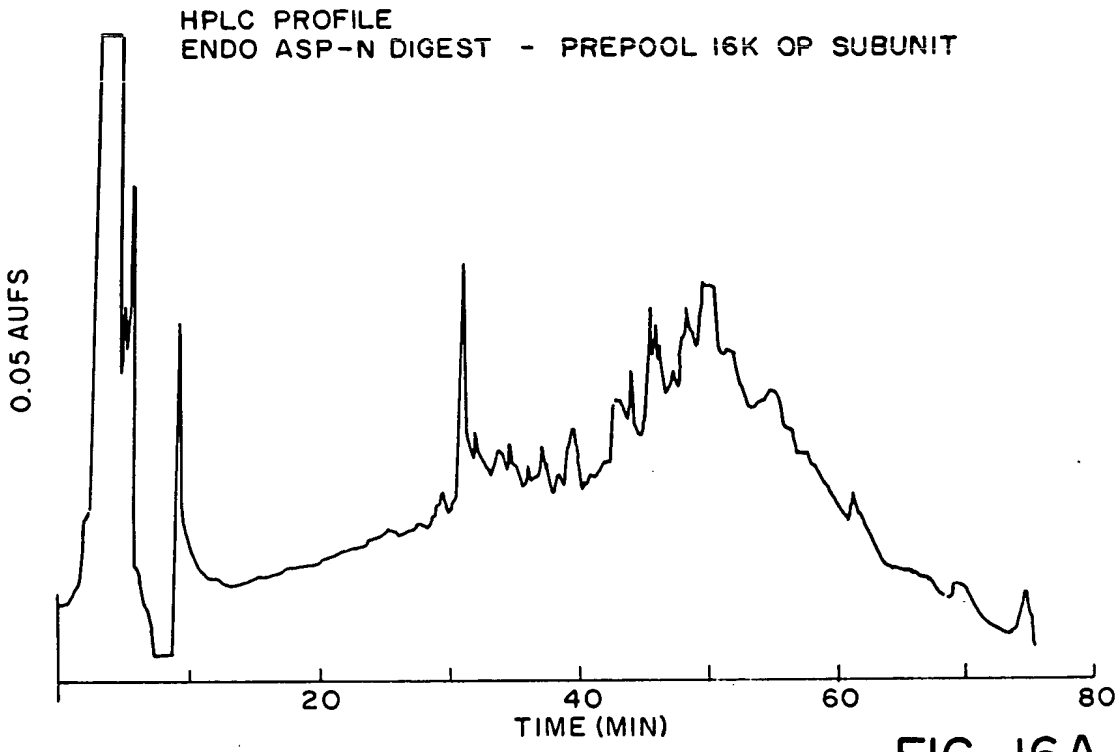


FIG. 16A

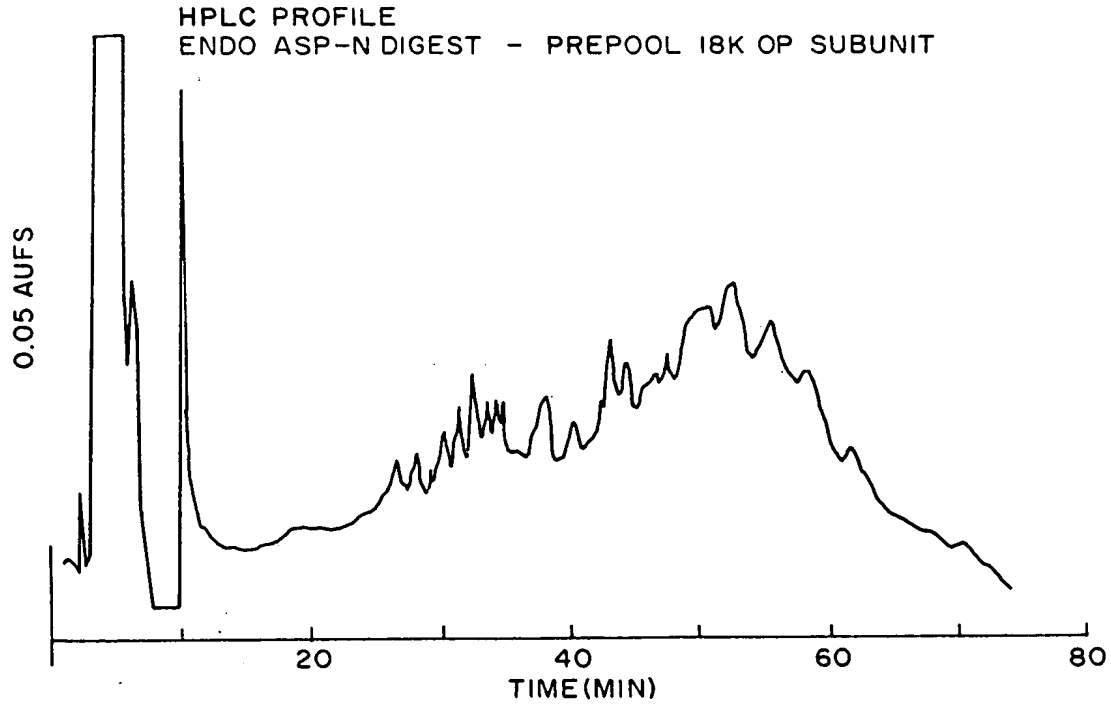


FIG. 16B

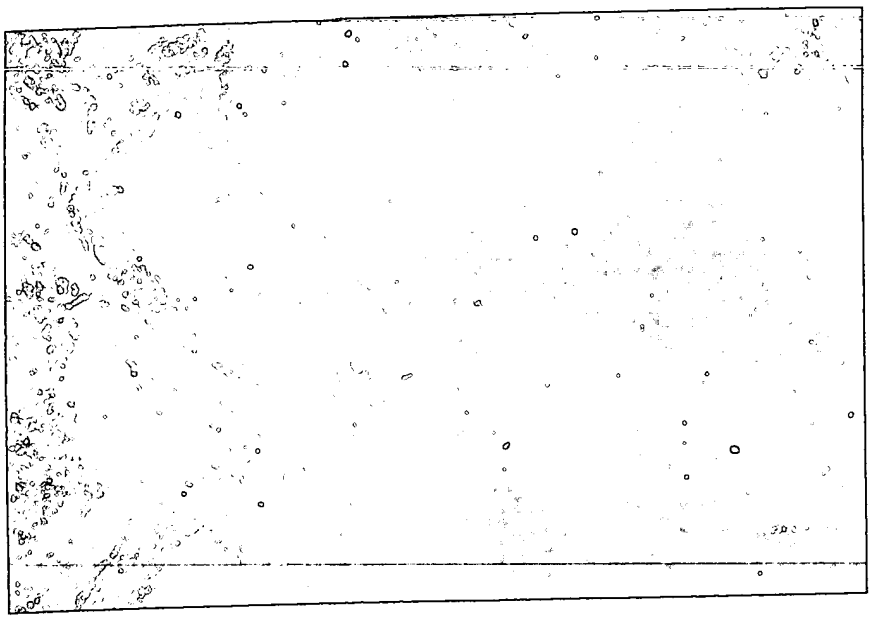


FIG. 17A

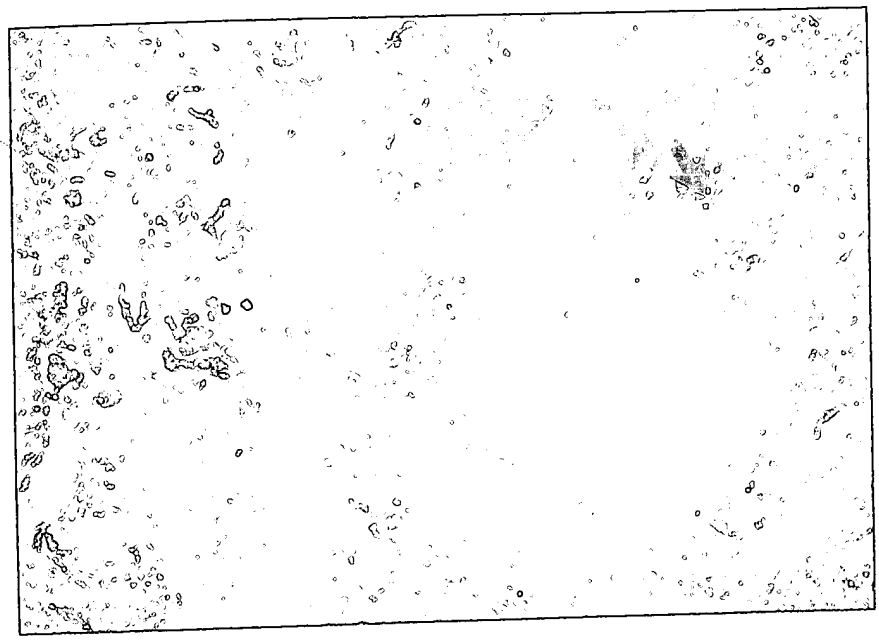


FIG. 17B

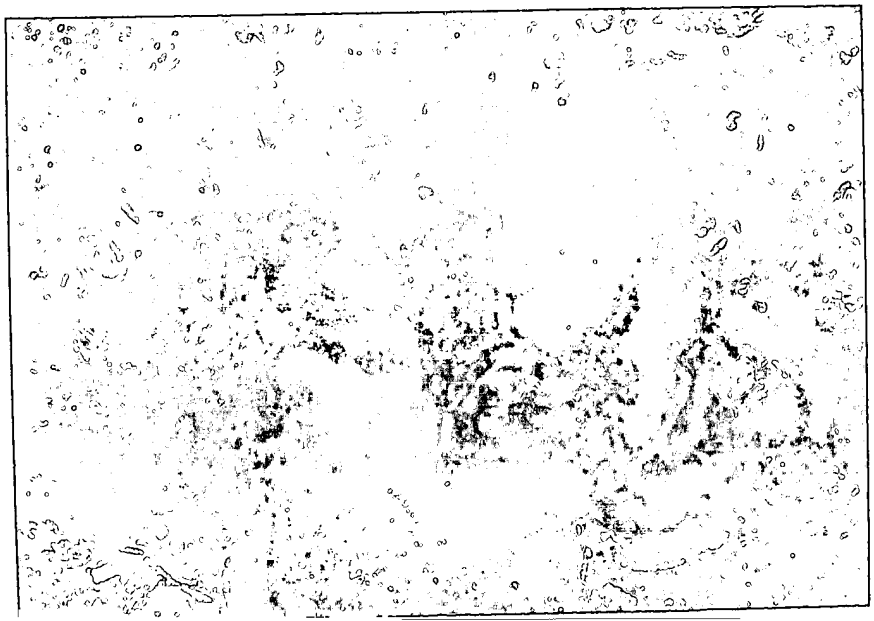


FIG. 17C

07/821988

COP1 COP3 COP4 COP5 COP7	VG1	DPP	OP1	CBMP2 a)	CBMP2 b)	CBMP3 (bov)	beta-Inhibin a)	beta-Inhibin b)	TGF-beta 1 2 3	MIS	alpha-Inhib	consensus choices
	C	C	C	C		C	C	C	C	C	C	c
	K	R	K	K	R	A	C	C	C	A	H	k,r
<P P P P P>	K	R	K	R		R	K	R	V L V	L	R	k,r
<N N N N N>	R	H	H	H		R	K	Q	R	R	V	h,k,r,q
<G G G G G>	H	S	E	P	S	Y	Q	Q	Q P P	E	A	p,s,e,q
L L L L L	L	L	L	L		L	F	F	L	L	L	l
Y Y Y Y Y	Y	Y	Y	Y		K	F	F	Y	S	N	y,f
V V V V V	V	V	V	V		V	V	I	I	V	I	v,i
D D D D D	E	D	S	D		D	S	D	D	D	S	d,e,s
F F F F F	F	F	F	F		F	F	F	F	L	F	f
Q Q S S S	K	S	R	S		A	K	R	R K R	R	Q	k,r,s
R R									K R Q	A		
D D D D D	D	D	D	D		D	D		D	E	E	d
V V V V V	V	V	L	V		I	I	I	L	R	L	v,l,i
G G G G G	G	G	G	G		G	G	G	G	S	G	g
W W W W W	W	W	W	W		W	W	W	W		W	w
D D D D N	Q	D	Q	N		S	N	N	K		E	q,n,d,e,s
D D D D D	N	D	D	D		E	D	D	-		R	d,e,n
W W W W W	W	W	W	W		W	W	W	W		W	w
I I I I I	V	I	I	I		I	I	I	I I V	V	I	i,v
I V V V V	I	V	I	V		I	I	I	H	L	V	i,v
A A A A A	A	A	A	A		S	A	A	E	I	Y	a,s
P P P P P	P	P	P	P		P	P	P	P	P	P	p
V P P P P	Q	L	E	P		K	S	T	K	E	P	e,q,p*
D G G G G	G	G	G	G		S	G	G	G	T	S	g,s
F Y Y Y Y	Y	Y	Y	Y		F	Y	Y	Y	Y	F	y,f
D Q Q Q H	M	D	V	H		D	H	Y	H N Y	Q	I	h,d,n,q,y*
A A A A A	A	A	A	A		A	A	G	A	A	F	a

FIG. 18-1

Y	F	F	F	F	::	N	Y	Y	F	:	Y	N	N	N	:	N	H	::	y,f,n
Y	Y	Y	Y	Y	::	Y	Y	Y	Y	:	Y	Y	Y	F	:	N	Y	::	y,f,n
C	C	C	C	C	::	C	C	C	C	:	C	C	C	C	:	C	C	::	c
S	S	S	H	H	::	Y	H	E	H	:	S	E	E	L	A	S:	Q	H	::	e,h,*
G	G	G	G	G	::	G	G	G	G	:	G	G	G	G	:	G	G	::	g
A	A	A	E	E	::	E	K	E	E	:	A	E	S	P	A	P:	V	G	::	e,a*
C	C	C	C	C	::	C	C	C	C	:	C	C	C	C	:	C	C	::	c
Q	Q	Q	P	P	::	P	P	A	P	:	Q	P	P	P	:	G	G	::	p,a,g,q
F	F	F	F	F	::	Y	F	F	F	:	F	S	A	Y	:	W	L	::	f,y
P	P	P	P	P	::	P	P	P	P	:	P	H	Y	I	L	L:	P	H	::	p
S	S	S	L	L	::	L	L	L	L	:	M	I	L	W	W	R:	Q	I	::	l,m,i
A	A	A	A	A	::	T	A	N	A	:	P	A	A	S		:	S	P	::	p,a,s,t
D	D	D	D	D	::	E	D	S	D	:	K	G	G			:	D	P	::	d,e,s,g*
H	H	H	H	H	::	I	H	Y	H	:	S	T	V	L		:	R	N	::	h,r,n, s*
F	F	F	F	L	::	L	F	M	L	:	L	S	P	L	S	A:		L	::	m,l,f,p,sa
N	N	N	N	N	::	N	N	N	N	:	K	G	G	D		:	N	S	::	n,k
S	S	S	S	S	::	G	S	A	S	:	P	S	S			:	P	L	::	s,a,p,g
T	T	T	T	T	::	S	T	T	T	:	S	S	A	T		:	R	P	::	t,s,a
N	N	N	N	N	::	N	N	N	N	:	N	L	S	Q	Q	T:	Y	V	::	n
					::					:		S	S			:	G	P	::	
					::					:		F	F			:	N	G	::	
H	H	H	H	H	::	H	H	H	H	:	H	H	H	Y	H	H:	H	A	::	h
					::					:		S	T			:			::	
A	A	A	A	A	::	A	A	A	A	:	A	T	A	S		:		P	::	a,t,s
V	V	V	V	V	::	I	V	I	I	:	T	V	V	K	R	T:	V	P	::	i,v,t
V	V	V	V	V	::	L	V	V	V	:	I	I	V	V		:	V	T	::	v,i,l
Q	Q	Q	Q	Q	::	Q	Q	Q	Q	:	Q	N	N	L		:	L	P	::	q,n
T	T	T	T	T	::	T	T	T	T	:	S	H	Q	A	S	G:	L	A	::	t, s,a,g
L	L	L	L	L	::	L	L	L	L	:	I	Y	Y	L		:	L	Q	::	l,i
V	V	V	V	V	::	V	V	V	V	:	V	R	R	Y		:	K	P	::	v
N	N	N	N	N	::	H	N	H	N	:	R	M	M	N		:	M	Y	::	h,n r

FIG. 18-2

N	N	N	S	S	::	S	N	F	S		:	A	R	R	Q	T	T:	Q	S	::	n,s *
M	M	M	V	V	::	I	N	I	V		:	V	G	G	H	I	L:	A	L	::	i,v,l,
N	N	N	N	N	::	E	N	N	N		:	G	H	L	N		:	R	L	::	n
					::						:	V	S	N			:	G		::	
					::						:	V					:	A		::	
P	P	P	S	S	::	P	P	P	S		:	P	P	P	P		:	A	P	::	p,s,a
G	G	G			::	E	G	E			:	G	F	G	G	E	E:	L	G	::	g,e
					::						:		A	T	A		:	A		::	
K	K	K	K	K	::	Q	K	T	K	S	:		N	K	S		:	R		::	k,q,t,s
V	V	V	I	I	::	I	V	V	I		:	I	L	V	A		:			::	i,v,l
P	P	P	P	P	::	P	P	P	P		:	P			A	S	S:	P	A	::	p,a,s
K	K	K	K	K	::	L	K	K	K		:	E	K	N			:		Q	::	k
P	P	P	A	A	::	P	A	A	A		:	P	S	S	P		:	P	P	::	a,p,s
C	C	C	C	C	::	C	C	C	C		:	C	C	C	C		:	C	C	::	c
C	C	C	C	C	::	C	C	C	C		:	C	C	C	C		:	C	C	::	c
V	V	V	V	V	::	V	V	A	V		:	V	V	I	V		:	V	A	::	v,a,i
P	P	P	P	P	::	P	P	P	P		:	P	P	P	P	S	P:	P	A	::	p,s,a
T	T	T	T	T	::	T	T	T	T		:	E	T	T	Q		:	T	L	::	t,e,q
E	E	E	E	E	::	K	Q	Q	E		:	K	K	K	A	D	D:	A	P	::	q,e,d,k*
L	L	L	L	L	::	M	L	L	L		:	M	L	L	L		:	Y	G	::	l,m
S	S	S	S	S	::	S	D	N	S		:	S	R	S	E		:	A	T	::	s,n e,d
A	A	A	A	A	::	P	S	A	A		:	S	P	T	P		:	G	M	::	a,s,p,t
I	I	I	I	I	::	I	V	I	I		:	L	M	M	L		:	K	R	::	i,l,m,v
S	S	S	S	S	::	S	A	S	S		:	S	S	S	P	T	T:	L	P	::	s,a,p,t
M	M	M	M	M	::	M	M	V	M		:	I	M	M	I		:	L	L	::	v,m,i,l
L	L	L	L	L	::	L	L	L	L		:	L	L	L	V	L	L:	I	H	::	l,v,i
Y	Y	Y	Y	Y	::	F	Y	Y	Y		:	F	Y	Y	Y		:	S	V	::	y,f
L	L	L	L	L	::	Y	L	F	L		:	F	Y	F	Y		:	L	R	::	f,l,y
D	D	D	D	D	::	D	N	D	D		:	D	D	D	V	I	V:	S	T	::	d,n
E	E	E	E	E	::	N	D	D	E		:	E	D	D	G		:	E	T	::	d,e,
N	N	N	N	N	::	N	Q	S	N	Y	:	N	G	E	R	K	R:	E	S	::	n,q,y*
E	E	E	E	E	::	D	S	S	E	D	:	K	Q	Y	K	T	T:	R	D	::	e,d,s,t

FIG. 18-3

K	K	K	K	K	::	N		T		N		K	:	N		N		N	P	:	I	G	::	n,k
V	V	V	V	V	::	V		V		V		V	:	V		I		I	K	:	S	G	::	v,i
V	V	V	V	V	::	V		V		I		V	:	V		I		V	V I V	:	A	Y	::	v,i
L	L	L	L	L	::	L		L		L		L	:	L		K		K	E	:	H	S	::	l
K	K	K	K	K	::	R		K		K		K	:	K		K		R	Q	:	H	F	::	k,r
N	N	N	N	N	::	H		N		K		N	:	V		D		D	L	:	V	K	::	n,d,k*
Y	Y	Y	Y	Y	::	Y		Y		Y		Y	:	Y		I		V		:		Y	::	y
Q	Q	Q	Q	Q	::	E		Q		R		Q	:	P		Q		P	S	:	P	E	::	q,e,p,r
					::								:							:		TVP	::	
E	E	E	E	E	::	N		E		N		D	E :	N		N		N	N	:	N	N	::	n,d,e
M	M	M	M	M	::	M		M		M		M	:	M		M		M	M	:	M	L	::	m
V	V	V	V	V	::	A		T		V		V	:	T		I		I	I I V	:	V	L	::	v,i,t,a
V	V	V	V	V	::	V		V		V		V	:	V		V		V	V	:	A	T	::	v
E	E	E	E	E	::	D		V		R		E	:	E		E		E	R K K	:	T	Q	::	e,d,r,k,
G	G	G	G	G	::	E		G		A		G	:	S		E		E	S	:	E	H	::	g,a,s,e
C	C	C	C	C	::	C		C		C		C	:	C		C		C	C	:	C	C	::	c
G	G	G	G	G	::	G		G		G		G	:	H		G		G	K	:	G	A	::	g,h
C	C	C	C	C	::	C		C		C		C	:	C		C		C	C	:	C	C	::	c
R	R	R	R	R	::	R		R		H		R	:	R		S		A	S	:	R	I	::	r,h,s,a,

FIG. 18-4

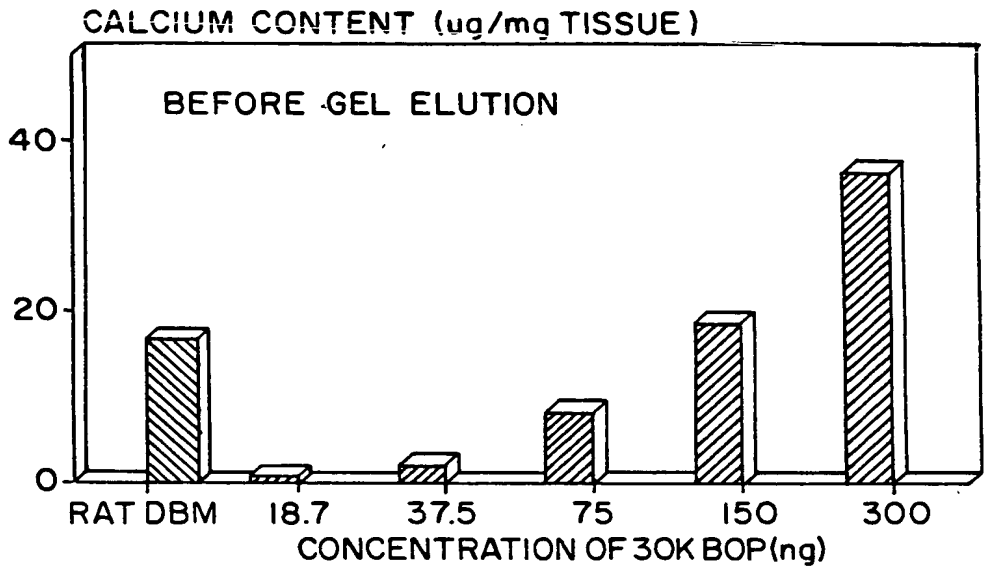


FIG. 20A

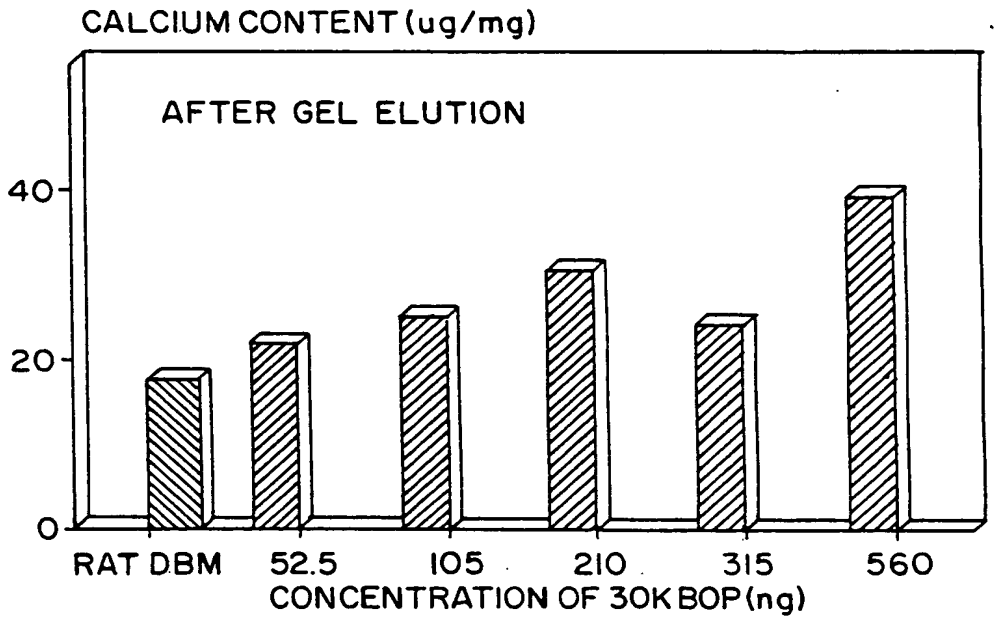


FIG. 20B

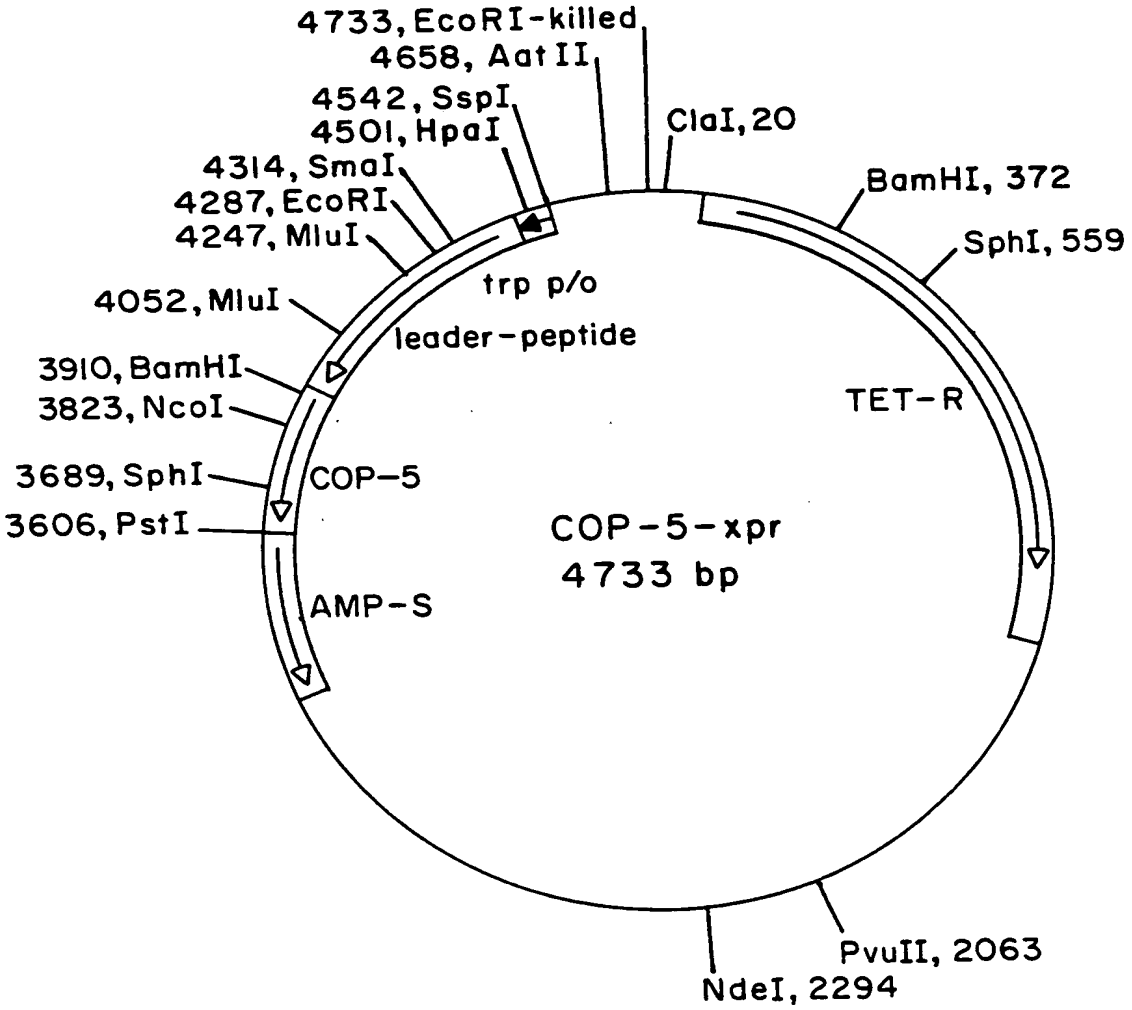


FIG. 21A

COP-5 fusion protein

```
          10         20         30         40         50
ATGAAAGCAATTTTCGTACTGAAAGGTTCACTGGACAGAGATCTGGACTC
 M  K  A  I  F  V  L  K  G  S  L  D  R  D  L  D  S
                                              BglII

          60         70         80         90        100
TCGTCTGGATCTGGACGTTCGTACCGACCACAAAGACCTGTCTGATCACC
  R  L  D  L  D  V  R  T  D  H  K  D  L  S  D  H

         110        120        130        140        150
TGGTTCTGGTCGACCTGGCTCGTAACGACCTGGCTCGTATCGTTACTCCC
L  V  L  V  D  L  A  R  N  D  L  A  R  I  V  T  P
         SalI                                      Sma

         160        170        180        190        200
GGGTCTCGTTACGTTGCGGATCTGGAATTCATGGCTGACAACAAATTCAA
 G  S  R  Y  V  A  D  L  E  F  M  A  D  N  K  F  N
I                          EcoRI

         210        220        230        240        250
CAAGGAACAGCAGAACGCGTTCTACGAGATCTTGCACCTGCCGAACCTGA
  K  E  Q  Q  N  A  F  Y  E  I  L  H  L  P  N  L
               MluI          BglII     BspMI+

         260        270        280        290        300
ACGAAGAGCAGCGTAACGGCTTCATCCAAAGCTTGAAGGATGAGCCCTCT
N  E  E  Q  R  N  G  F  I  Q  S  L  K  D  E  P  S
                                HindIII

         310        320        330        340        350
CAGTCTGCGAATCTGCTAGCGGATGCCAAGAAACTGAACGATGCGCAGGC
 Q  S  A  N  L  L  A  D  A  K  K  L  N  D  A  Q  A
               NheI                              FspI

         360        370        380        390        400
ACCGAAATCGGATCAGGGGCAATTCATGGCTGACAACAAATTCAACAAGG
  P  K  S  D  Q  G  Q  F  M  A  D  N  K  F  N  K

         410        420        430        440        450
AACAGCAGAACGCGTTCTACGAGATCTTGCACCTGCCGAACCTGAACGAA
E  Q  Q  N  A  F  Y  E  I  L  H  L  P  N  L  N  E
          MluI          BglII     BspMI+

         460        470        480        490        500
GAGCAGCGTAACGGCTTCATCCAAAGCTTGAAGGATGAGCCCTCTCAGTC
 E  Q  R  N  G  F  I  Q  S  L  K  D  E  P  S  Q  S
                          HindIII
```

FIG. 21B-1

```
       510        520        530        540        550
TGCGAATCTGCTAGCGGATGCCAAGAAACTGAACGATGCGCAGGCACCGA
  A  N  L  L  A  D  A  K  K  L  N  D  A  Q  A  P
        NheI                              FspI

       560        570        580        590        600
AGGATCCTAATGGGCTGTACGTCGACTTCAGCGACGTGGGCTGGGACGAC
K  D  P  N  G  L  Y  V  D  F  S  D  V  G  W  D  D
 BamHI              SalI

       610        620        630        640        650
TGGATTGTGGCCCCACCAGGCTACCAGGCCTTCTACTGCCATGGCGAATG
 W  I  V  A  P  P  G  Y  Q  A  F  Y  C  H  G  E  C
                          StuI        NcoI   BsmI+

       660        670        680        690        700
CCCTTTCCCGCTAGCGGATCACTTCAACAGCACCAACCACGCCGTGGTGC
  P  F  P  L  A  D  H  F  N  S  T  N  H  A  V  V
        NheI                              DraIII
                                          PflMI

       710        720        730        740        750
AGACCCTGGTGAACTCTGTCAACTCCAAGATCCCTAAGGCTTGCTGCGTG
Q  T  L  V  N  S  V  N  S  K  I  P  K  A  C  C  V
                                 MstII

       760        770        780        790        800
CCCACCGAGCTGTCCGCCATCAGCATGCTGTACCTGGACGAGAATGAGAA
 P  T  E  L  S  A  I  S  M  L  Y  L  D  E  N  E  K
                       SphI

       810        820        830        840        850
GGTGGTGCTGAAGAACTACCAGGAGATGGTAGTAGAGGGCTGCGGCTGCC
  V  V  L  K  N  Y  Q  E  M  V  V  E  G  C  G  C
                    PflMI

       860
GCTAACTGCAG
R  *
     PstI
```

FIG. 21B-2

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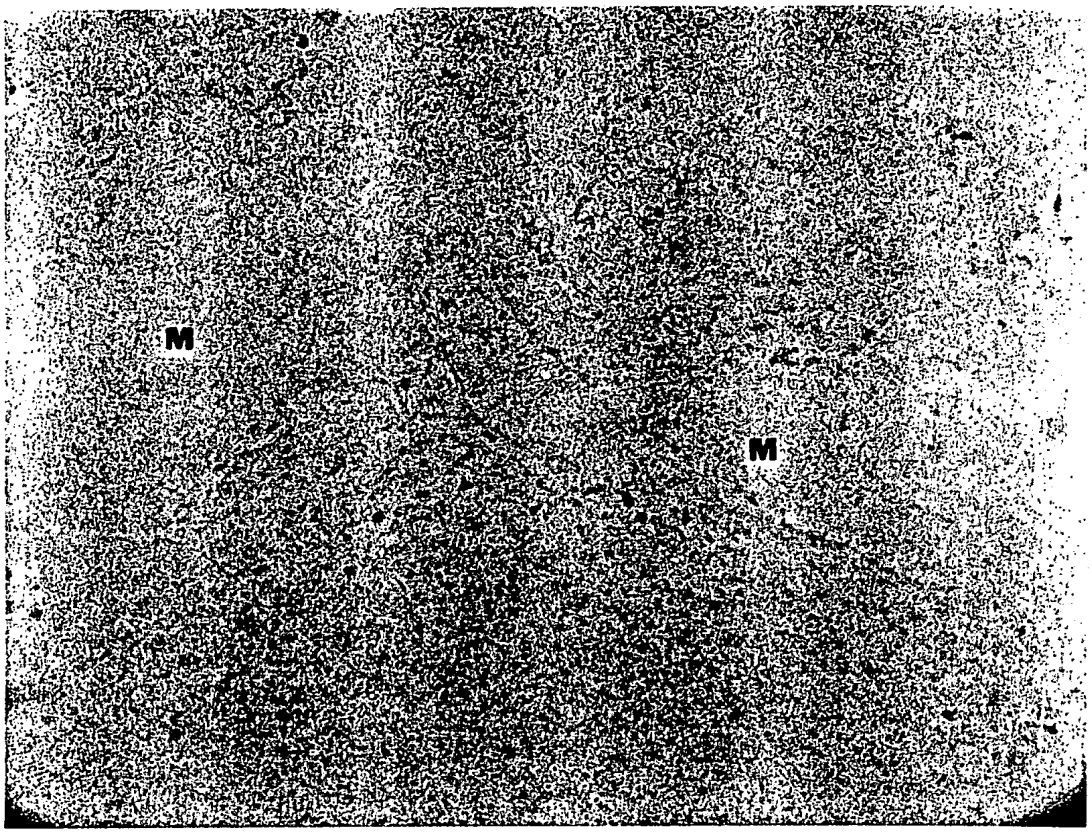

FIG. 22A

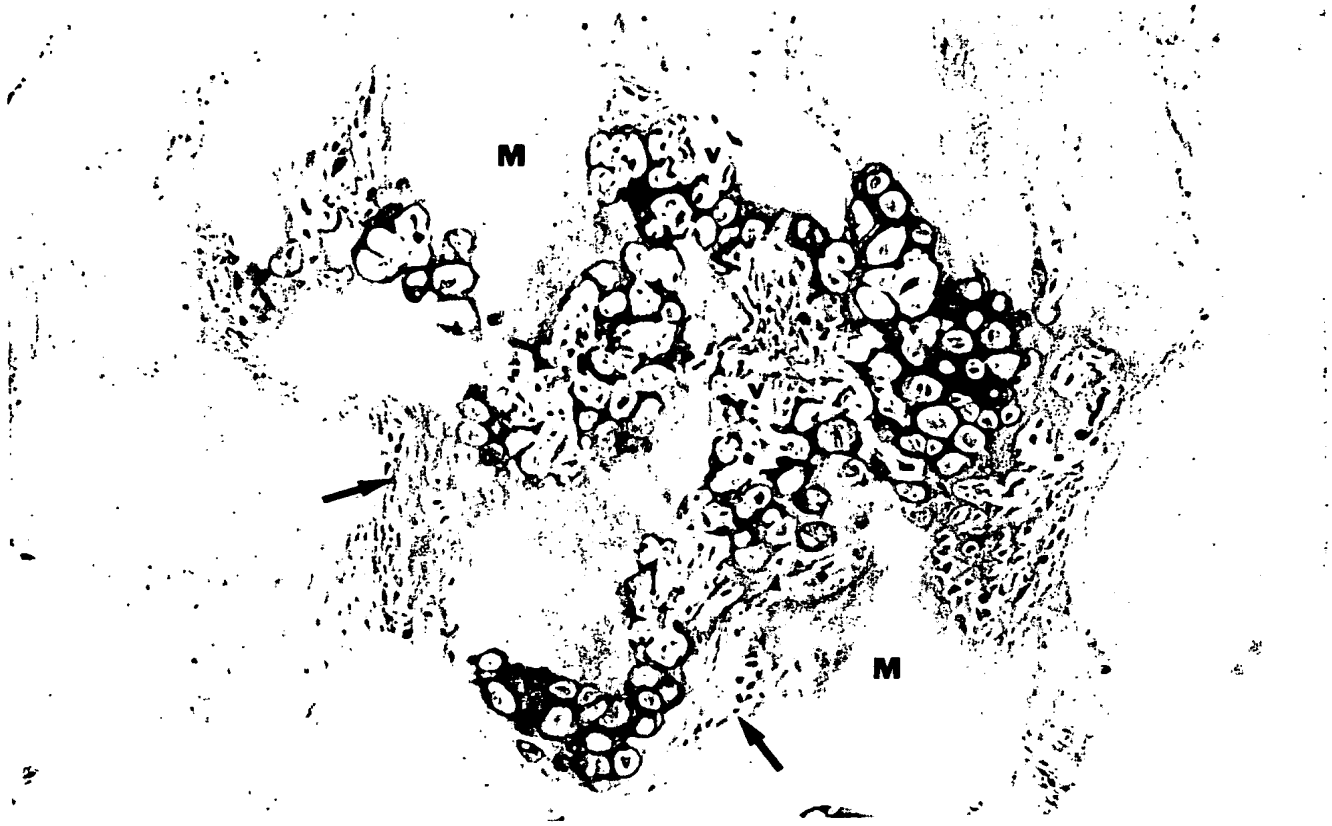

FIG. 22B